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Sequence Listing was accepted.

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Reviewer: Keisha Douglas

Timestamp: Thu Aug 30 16:03:23 EDT 2007

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Application No: 10764131 Version No: 2.0

Input Set:

Output Set:

Started: 2007-08-20 08:38:33.548
Finished: 2007-08-20 08:38:34.020
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 472 ms
Total Warnings: 5
Total Errors: 0
No. of SeqIDs Defined: 5
Actual SeqID Count: 5

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)

SEQUENCE LISTING

<110> KELER, TIBOR
GOLDSTEIN, JOEL
GRAZIANO, ROBERT
DEO, YASHWANT M.

<120> CELLS EXPRESSING ANTI-FC RECEPTOR BINDING COMPONENTS

<130> CDJ-099CN

<140> 10764131

<141> 2004-01-23

<150> 09/203,958

<151> 1998-12-02

<150> 60/067,232

<151> 1997-12-02

<160> 5

<170> PatentIn Ver. 3.3

<210> 1

<211> 1132

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<220>

<221> CDS

<222> (74)..(1129)

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ggggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg 109
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
1 5 10

ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat 157
Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
15 20 25

tat gct ggg gcc cag ccg gcc aga tct gat atc cag ctg acc cag agc 205
Tyr Ala Gly Ala Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser
30 35 40

cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt 253
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
45 50 55 60

aag tcc agt caa agt gtt tta tac agt tca aat cag aag aac tac ttg	301
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu	
65 70 75	
gcc tgg tac cag cag aag cca ggt aag gct cca aag ctg ctg atc tac	349
Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr	
80 85 90	
tgg gca tcc act agg gaa tct ggt gtg cca agc aga ttc agc ggt agc	397
Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser	
95 100 105	
ggg agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag cca gag	445
Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu	
110 115 120	
gac atc gcc acc tac tac tgc cat caa tac ctc tcc tcg tgg acg ttc	493
Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe	
125 130 135 140	
ggc caa ggg acc aag gtg gaa atc aag agc tct ggc ggt ggc ggc tcc	541
Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser	
145 150 155	
gga ggt gga ggc agc gga ggg ggt gga tcc gag gtc caa ctg gtg gag	589
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu	
160 165 170	
agc ggt gga ggt gtt gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc	637
Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys	
175 180 185	
tcc tcg tct ggc ttc att ttc agt gac aat tac atg tat tgg gtg aga	685
Ser Ser Ser Gly Phe Ile Phe Ser Asp Asn Tyr Met Tyr Trp Val Arg	
190 195 200	
cag gca cct gga aaa ggt ctt gag tgg gtt gca acc att agt gat ggt	733
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Gly	
205 210 215 220	
ggg agt tac acc tac tat cca gac agt gtg aag gga aga ttt aca ata	781
Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile	
225 230 235	
tcg aga gac aac agc aag aac aca ttg ttc ctg caa atg gac agc ctg	829
Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu	
240 245 250	
aga ccc gaa gac acc ggg gtc tat ttt tgt gca aga ggc tac tat agg	877
Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Gly Tyr Tyr Arg	
255 260 265	
tac gag ggg gct atg gac tac tgg ggc caa ggg acc ccg gtc acc gtc	925
Tyr Glu Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val	
270 275 280	
tcc tca ccg cgg ctg cag gtc gac gaa caa aaa ctc atc tca gaa gag	973

Ser Ser Pro Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu
 285 290 295 300

gat ctg aat gct gtg ggc cag gac acg cag gag gtc atc gtg gtg cca 1021
 Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro
 305 310 315

cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc atc ctg gcc ctg 1069
 His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu
 320 325 330

gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc atg ctt tgg cag 1117
 Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln
 335 340 345

aag aag cca cgt tag 1132
 Lys Lys Pro Arg
 350

<210> 2
 <211> 1135
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 construct

<220>
 <221> CDS
 <222> (74)..(1132)

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ggggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg 109
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
 1 5 10

ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat 157
 Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
 15 20 25

tat gct ggg gcc cag ccg gcc aga tct gag atc cag ctg cag cag act 205
 Tyr Ala Gly Ala Gln Pro Ala Arg Ser Glu Ile Gln Leu Gln Gln Thr
 30 35 40

gga cct gag ctg gtg aag cct ggg gct tca gtg aag ata tcc tgc aag 253
 Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys
 45 50 55 60

gct tct ggt tat tca ttc act gac tac atc ata ttt tgg gtg aag cag 301
 Ala Ser Gly Tyr Ser Phe Thr Asp Tyr Ile Ile Phe Trp Val Lys Gln
 65 70 75

agc cat gga aag agc ctt gag tgg act gga aat att aat cct tac tat 349

Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Thr	Gly	Asn	Ile	Asn	Pro	Tyr	Tyr		
			80						85					90			
ggt	agt	act	agc	tac	aat	ctg	aag	ttc	aag	ggc	aag	gcc	aca	ttg	act	397	
Gly	Ser	Thr	Ser	Tyr	Asn	Leu	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr		
			95				100					105					
gta	gac	aaa	tct	tcc	agc	aca	gcc	tac	atg	cag	ctc	aac	agt	ctg	aca	445	
Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Asn	Ser	Leu	Thr		
			110				115					120					
tct	gag	gac	tct	gca	gtc	tat	tac	tgt	gta	aga	gga	gtt	tat	tac	tac	493	
Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Val	Arg	Gly	Val	Tyr	Tyr	Tyr		
125					130					135					140		
ggt	agt	agc	tac	gag	gcg	ttt	cct	tac	tgg	ggc	caa	ggg	act	ctg	gtc	541	
Gly	Ser	Ser	Tyr	Glu	Ala	Phe	Pro	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val		
				145					150					155			
act	gtc	tct	gca	gga	ggg	ggc	ggc	tcc	gga	gga	ggg	ggc	agc	gga	ggg	589	
Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly		
			160					165					170				
ggc	gga	tcc	gat	gtt	gtg	atg	acc	cag	act	cca	ctc	act	ttg	tcg	att	637	
Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Thr	Leu	Ser	Ile		
			175				180					185					
acc	att	gga	caa	cca	gcc	tcc	atc	tct	tgc	aag	tca	agt	cag	agc	ctc	685	
Thr	Ile	Gly	Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu		
			190				195				200						
tta	gat	agt	gat	gga	aag	aca	tat	ttg	aat	tgg	ttg	tta	cag	agg	cca	733	
Leu	Asp	Ser	Asp	Gly	Lys	Thr	Tyr	Leu	Asn	Trp	Leu	Leu	Gln	Arg	Pro		
205					210					215					220		
ggc	cag	tct	cca	acg	cgc	cta	atc	tat	ctg	gtg	tct	aaa	ctg	gac	tct	781	
Gly	Gln	Ser	Pro	Thr	Arg	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Asp	Ser		
				225					230				235				
gga	gtc	cct	gac	agg	ttc	act	ggc	agt	gga	tca	ggg	aca	gat	ttc	aca	829	
Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr		
			240					245					250				
ctg	aaa	atc	agc	aga	gtg	gag	gct	gag	gat	ttg	gga	att	tat	tat	tgc	877	
Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Ile	Tyr	Tyr	Cys		
			255				260					265					
tgg	caa	ggg	gca	cat	ttt	cct	cag	acg	ttc	ggg	gga	ggc	acc	aag	ctg	925	
Trp	Gln	Gly	Ala	His	Phe	Pro	Gln	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu		
			270				275				280						
gaa	atc	aaa	ccg	cgg	ctg	cag	gtc	gac	gaa	caa	aaa	ctc	atc	tca	gaa	973	
Glu	Ile	Lys	Pro	Arg	Leu	Gln	Val	Asp	Glu	Gln	Lys	Leu	Ile	Ser	Glu		
285					290					295					300		
gag	gat	ctg	aat	gct	gtg	ggc	cag	gac	acg	cag	gag	gtc	atc	gtg	gtg	1021	
Glu	Asp	Leu	Asn	Ala	Val	Gly	Gln	Asp	Thr	Gln	Glu	Val	Ile	Val	Val		

305	310	315	
cca cac tcc ttg ccc ttt aag gtg	gtg gtg atc tca gcc atc ctg gcc	1069	
Pro His Ser Leu Pro Phe Lys Val	Val Val Ile Ser Ala Ile Leu Ala		
320	325 330		
ctg gtg gtg ctc acc atc atc tcc ctt	atc atc ctc atc atg ctt tgg	1117	
Leu Val Val Leu Thr Ile Ile Ser Leu	Ile Ile Leu Ile Met Leu Trp		
335	340 345		
cag aag aag cca cgt tag		1135	
Gln Lys Lys Pro Arg			
350			

<210> 3

<211> 352

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 3

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Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala	
20 25 30	
Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu	
35 40 45	
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln	
50 55 60	
Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln	
65 70 75 80	
Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr	
85 90 95	
Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr	
100 105 110	
Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr	
115 120 125	
Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe Gly Gln Gly Thr	
130 135 140	
Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
145 150 155 160	
Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly	
165 170 175	

Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ser	Ser	Gly
180				185				190							
Phe	Ile	Phe	Ser	Asp	Asn	Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly
195				200				205							
Lys	Gly	Leu	Glu	Trp	Val	Ala	Thr	Ile	Ser	Asp	Gly	Gly	Ser	Tyr	Thr
210				215				220							
Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn
225				230				235				240			
Ser	Lys	Asn	Thr	Leu	Phe	Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp
245				250				255							
Thr	Gly	Val	Tyr	Phe	Cys	Ala	Arg	Gly	Tyr	Tyr	Arg	Tyr	Glu	Gly	Ala
260				265				270							
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Pro	Val	Thr	Val	Ser	Ser	Pro	Arg
275				280				285							
Leu	Gln	Val	Asp	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ala
290				295				300							
Val	Gly	Gln	Asp	Thr	Gln	Glu	Val	Ile	Val	Val	Pro	His	Ser	Leu	Pro
305				310				315				320			
Phe	Lys	Val	Val	Val	Ile	Ser	Ala	Ile	Leu	Ala	Leu	Val	Val	Leu	Thr
325				330				335							
Ile	Ile	Ser	Leu	Ile	Ile	Leu	Ile	Met	Leu	Trp	Gln	Lys	Lys	Pro	Arg
340				345				350							
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<211> 353															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Description of Artificial Sequence: Synthetic construct															
<400> 4															
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Gly	Ser	Thr	Gly	Asp	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Gly	Ala
20				25				30							
Gln	Pro	Ala	Arg	Ser	Glu	Ile	Gln	Leu	Gln	Gln	Thr	Gly	Pro	Glu	Leu
35				40				45							
Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
50				55				60							

Ser Phe Thr Asp Tyr Ile Ile Phe Trp Val Lys Gln Ser His Gly Lys
65 70 75 80

Ser Leu Glu Trp Thr Gly Asn Ile Asn Pro Tyr Tyr Gly Ser Thr Ser
85 90 95

Tyr Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser
100 105 110

Ser Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser
115 120 125

Ala Val Tyr Tyr Cys Val Arg Gly Val Tyr Tyr Tyr Gly Ser Ser Tyr
130 135 140

Glu Ala Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
165 170 175

Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Ile Thr Ile Gly Gln
180 185 190

Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp
195 200 205

Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro
210 215 220

Thr Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp
225 230 235 240

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
245 250 255

Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly Ala
260 265 270

His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Pro
275 280 285

Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
290 295 300

Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
305 310 315 320

Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
325 330 335

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
340 345 350

Arg

<210> 5

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 5

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